Figure 1

exon II		
megsin	ATTGATAAGgtcag	tacagTTGCTTCAT
PAI2	ATGGCCAAGgtgag	tgcagGTGCTTCAG
exon III		
megsin	AATAGTCAGgtaaa	aacagTCAGGGCTC
PAI2	ATTTTGCAGgtatc	tcaagGCACAAGCT
exon IV		
megsin	TTTCATAAGgtaag	tatagGACTACATT
PAI2	TTCCGGGAAgtaag	aaaagGAATATATT
exon V		
megsin	ACATGgtgag	aaaagGCAAA
PAI2	CAAACCAAAGgtaaa	ctgtagGCAAAATCC
exon IV		
megsin	CCAAGgtatg	ttcagTGCTC
PAI2	GTAAACTCGgtatg	attagGCTCAGCGC
exon IV		
megsin	CTGAAgtaag	tacagATTGA
PAI2	TTGGAGCTGgtaag	tgcagCTGGAAAGT

Figure 2

• Promoter region 1431 bp (-1431~-1)

-1431

a ctttatatcc tcagtaggta agaaatacaa aggatatggg attcaaaata -1381
ttcagcctat gaacactgca attagaatat ggagaacagg gaatccattt gtaggctcat -1321
ttttttttta tattaacaac aaccttctcc ttcagaaagt tcaccacaac tgctaaatca -1261
aaattaaatt tcagggattt tctgcaactt tacttttctc tatgattatt catctcataa -1201
acaatcatgg aggtgagcaa taactacttt attcgatttt ggataagtta acaggacccc -1141
cttcttcctg ggaaggaggc aaaattgcac aaaattgaga ggcgagcaac tgtaagatga -1081
tggtaccttc taattccaat agctttttac aatagagaac ccagttactt ggataaatgt -1021
tggctgtact tttgaaaaca ctcaggcaga aggaccaggc ttgcagtcat ttccatgcat -961
agcaggtgaa ggtaggtgca acatacagct caacctcatg atgctacggc cagaaactga -901
aatgtgtttt tgcccctgtg tggcatgttc tgatggcaaa ggtgtaggca accaactagg -841
cccaacctac ctttccctac acctggtcac ttttcaaagt gcaaacccac tttaacaaac -781
tctagcctgt attataggag gaaggatctg ggtggtgcag acgtggcttt ccattgccag -721
atcagaaggg tggaggagag actggcagga tgacaagaat gaatgaacac accaagtttc -661
agctcctatc tgaagctgct cagttcaggt aagcatttag agaagccagt tgcaataact -601
aacagggcaa atgtttctct ggaaaattcc aagccagaga aaattgagaa aaagagggaa -541
ggatggaaag cagtacaaag agaagccagc tcaaaaggtt agaggtccag atgaaaatct -481
gagattggag aatgataaaa aacattgtgt gagattctat tttaggtcat tatgctaggg -421
aaatttacac aggatagggt tgaaagaaat taggctataa gatgagtggc aagttgcaat -361
aaaatggcac cctaaactca ccaagtcact gttgtcactg ctatcttgcc ttagttgatt -301
tgatgtctag ttagtctatt tgtgtgtttc tcacagaaga gtatgtcttg acccaggctg -241
acagatactg ttgattctga aatttgtttt tatggttatg ttaaaaccat tgtcattata -181
agaaacagag atgggaatat tgcctcctga aatctgattc acatacaaac tgaatgaact -121
acataacaac caccttagtc agatactact ttgaaacctg gttcaaaacc taaatgctta -61
taagarrctt gagagacagt gctgtgctct gagtcatagg gaagccatcc cagaagccag -1

• 5'-Untranslated region (5'-UTR) 181 bp (+1~+181)

gtctacttat caataagcag ctgcctgtgc agagtgcagg ctgcaccttt ggacagcctt 60
taaaactgaa ttctcagaat tttagaacaa atttttgtct agaaatgctg actttggttc 120
attaggtagt ggtaaaacag gctcccttcg aagctctcct tcatcacctt cctaagtgca 180
t 181

Figure 3

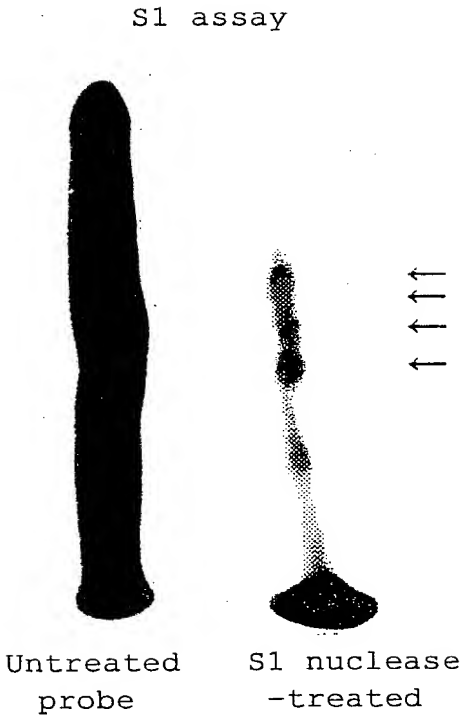


Figure 4

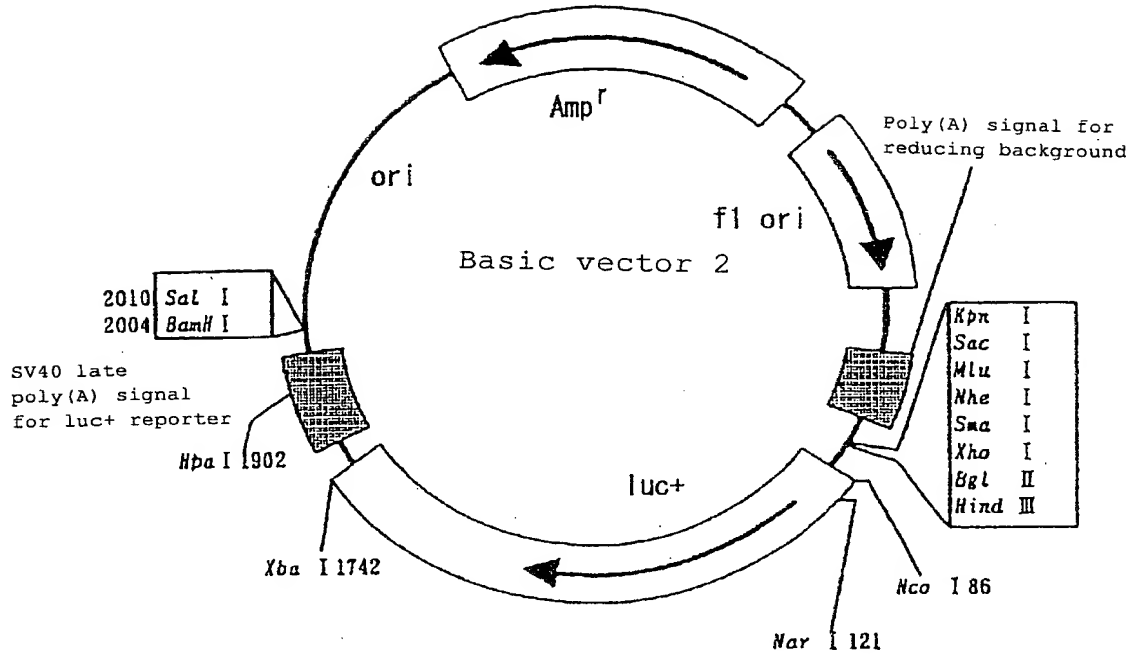

Amp r
ori
f1 ori
Basic vector 2
Poly(A) signal for reducing background
2010 Sal I
2004 BamH I
SV40 late poly(A) signal for luc+ reporter
Hpa I 1902
Xba I 1742
luc+
Nar I 121
Nco I 86
Kpn I
Sac I
Mlu I
Nhe I
Sma I
Xho I
Bgl II
Hind III

Figure 5

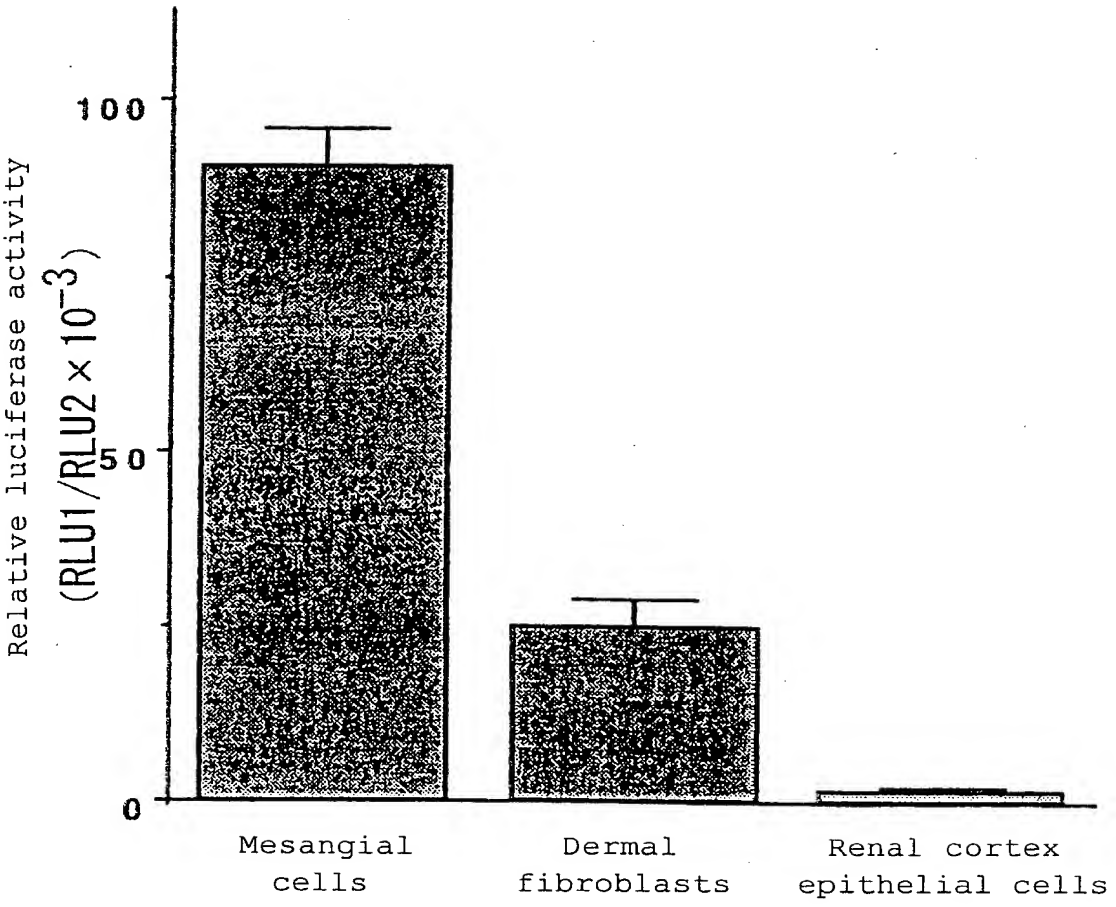

Relative luciferase activity
(RLU1/RLU2 × 10⁻³)
100
50
0
Mesangial cells
Dermal fibroblasts
Renal cortex epithelial cells

Figure 6

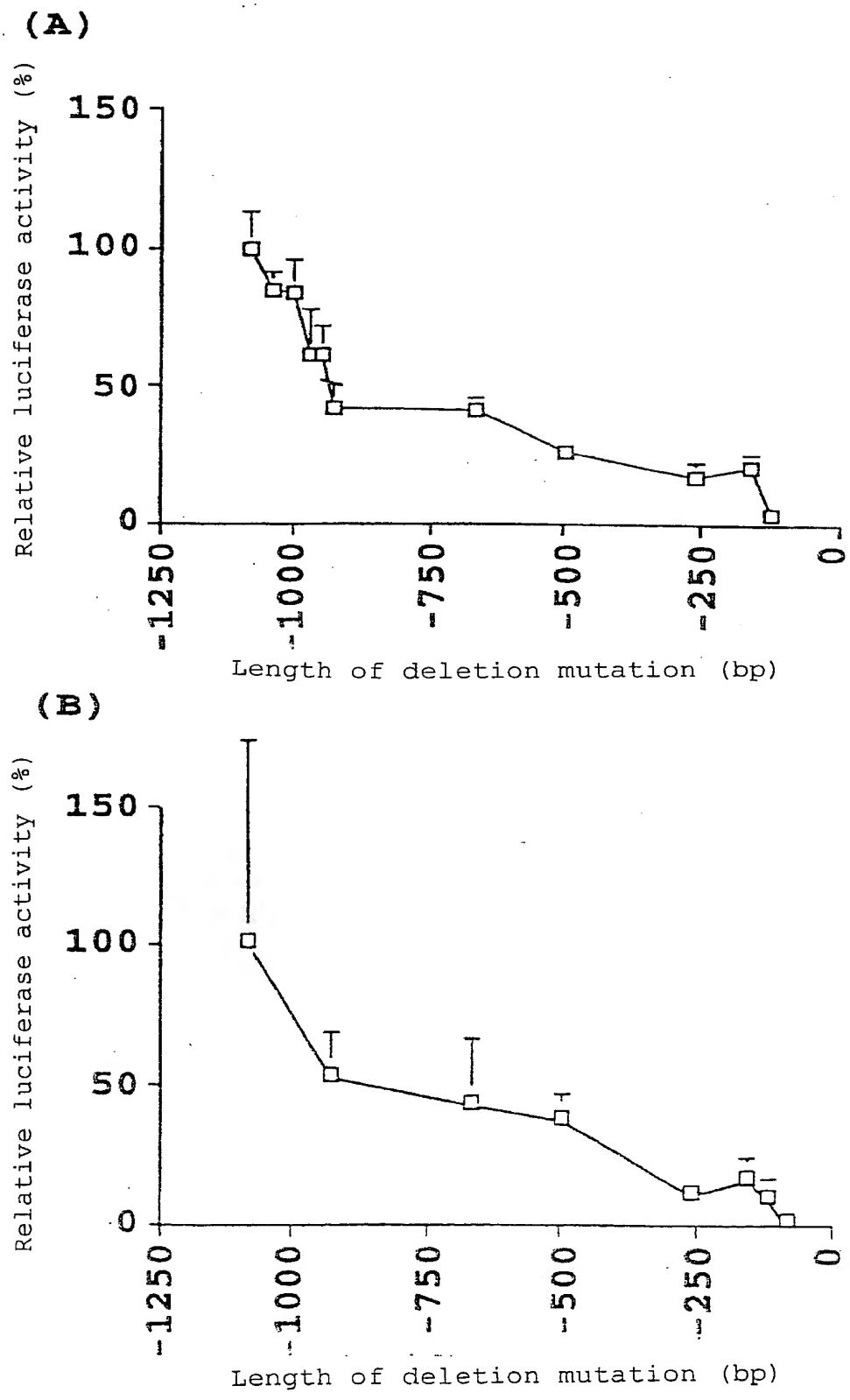

(A)
Relative luciferase activity (%)
150
100
50
0
-1250
-1000
-750
-500
-250
0
Length of deletion mutation (bp)
(B)
Relative luciferase activity (%)
150
100
50
0
-1250
-1000
-750
-500
-250
0
Length of deletion mutation (bp)

Figure 7

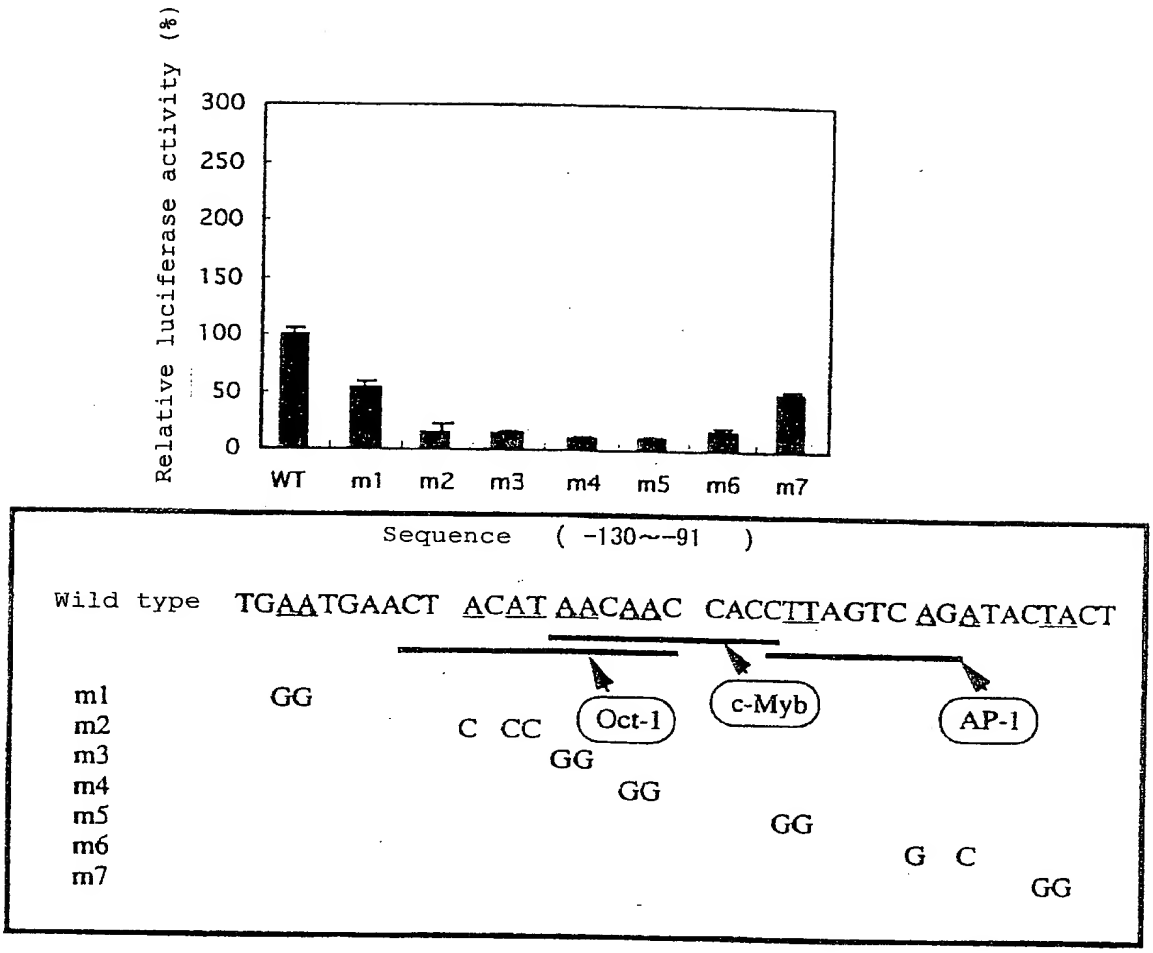
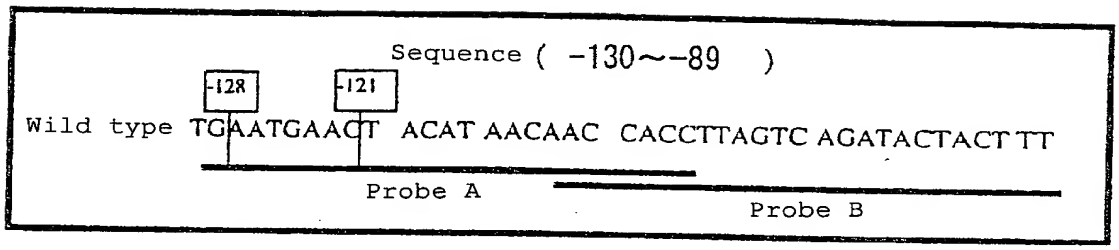
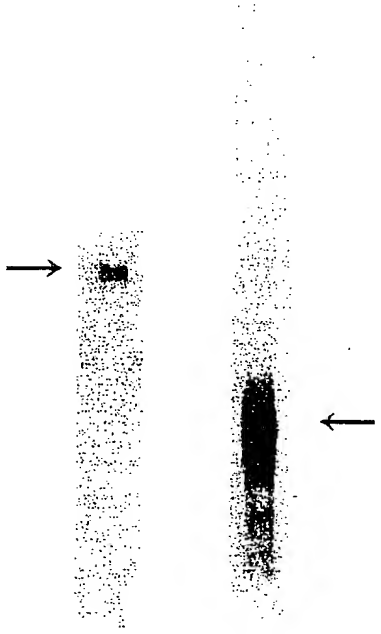

Relative luciferase activity (%)
300
250
200
150
100
50
0
WT
m1
m2
m3
m4
m5
m6
m7
Sequence (-130~-91)
Wild type TGAATGAACT ACAT AACAAC CACCTTAGTC AGATACTACT
Oct-1
c-Myb
AP-1
m1 GG
m2 C CC
m3 GG
m4 GG
m5 GG
m6 G C
m7 GG

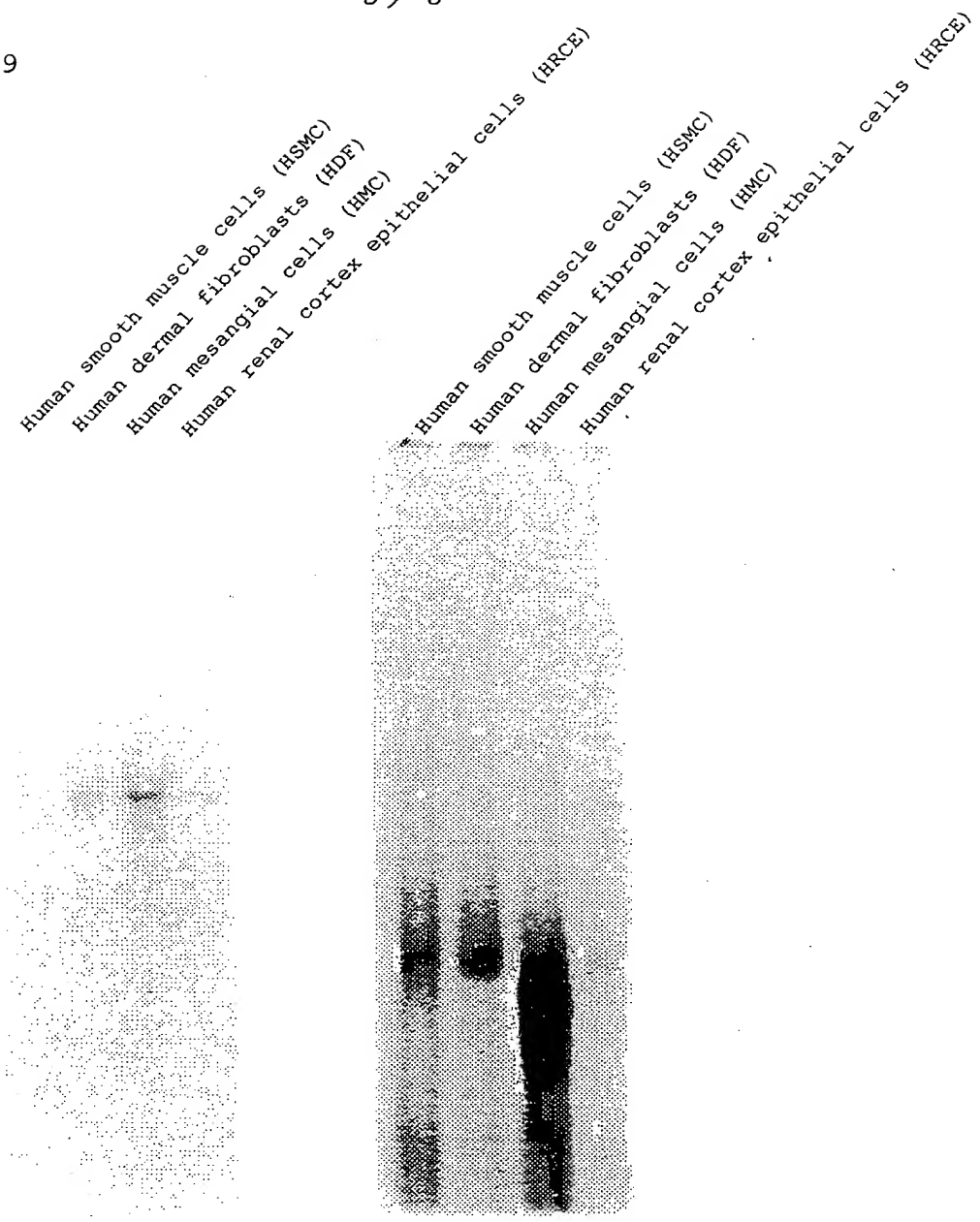
Figure 8





Probe A Probe B

Figure 9


Human smooth muscle cells (HSMC)
Human dermal fibroblasts (HDF)
Human mesangial cells (HMC)
Human renal cortex epithelial cells (HRCE)
Human smooth muscle cells (HSMC)
Human dermal fibroblasts (HDF)
Human mesangial cells (HMC)
Human renal cortex epithelial cells (HRCE)
Probe A
Probe B